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CORRECTED SEQUENCE LISTING

<110> Conseiller, Emmanuel
Debussche, Laurent
Gallagher, William

<120> Polypeptide (MBP1) Capable Of Interacting With Oncogenic Mutants Of The P53 Protein

<130> ST98033

<140> 09/829,936

<141> 2001-04-11

<150> FR9812754

<151> 1998-10-12

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide 5'-1(p53)

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agatctgtat ggaggagccg cag

23

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<211> 29

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<210> 4

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<223> oligonucleotide w248 3'

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gggcctccag ttcat 15

<210> 5

<211> 15

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<223> oligonucleotide H273 3'

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acaaacatgc acctc 15

<210> 6

<211> 15

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide G281 3'

<400> 6
gcgccggcctt ctc

15

<210> 7

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide 5'-73

<400> 7
agatctgtgt ggcccttgca cca

23

<210> 8

<211> 1021

<212> DNA

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<220>
<223> Murine MBP1 C-term fragment

<220>
<221> CDS
<222> (1)..(885)

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Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

48

ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

96

ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

144

aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

192

tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

240

aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc

288

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
 85 90 95
 gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc aac 336
 Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
 100 105 110
 gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg ctg 384
 Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
 115 120 125
 gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca cac 432
 Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
 130 135 140
 caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac cgc 480
 Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
 145 150 155 160
 tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca gac 528
 Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
 165 170 175
 aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag cct 576
 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
 180 185 190
 tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt gtg 624
 Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
 195 200 205
 cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt gcc 672
 Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
 210 215 220
 tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc tac 720
 Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
 225 230 235 240
 att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg cca 768
 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
 245 250 255
 gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg 816
 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
 260 265 270
 aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg gtc 864
 Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
 275 280 285
 ttt gtg gga gcc tat acc ttc tgaagaccct caggaaaggg ccatgtgggg 915
 Phe Val Gly Ala Tyr Thr Phe
 290 295
 gccccttccc cctccatag cttaaaggcagc cccggggggcc tagggatgac cgttctgctt 975
 aaaggaacta tgatgtgaag gacaataaag ggagaaaagaa ggaaaa 1021

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<211> 295

<212> PRT

<213> Artificial sequence

<220>

<223> Murine MBP1 C-term fragment

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Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
180 185 190

Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
Page 5

210

215

220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
275 280 285

Phe Val Gly Ala Tyr Thr Phe
290 295

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotide c-myc 5'

<400> 10

gatccatgga gcagaagctg atctccgagg aggacctga

39

<210> 11

<211> 39

<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotide c-myc 3'

<400> 11

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39

<210> 12

<211> 45

<212> DNA

<213> Artificial Sequence

<220>
<223> 5' MCS oligonucleotide

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<210> 13

<211> 37

<212> DNA

<213> Artificial Sequence

<220>
<223> 3' MCS oligonucleotide

<400> 13
cgcggccgca cccgggaattt gcatgcaggt cgaccga 37

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotide 3' mMBP1

<400> 14
cggtactggc agaggtaact gg 22

<210> 15

<211> 1513

<212> DNA

<213> Artificial Sequence

<220>
<223> MBP1 murine (complete sequence)

<220>

<221> CDS

<222> (49)..(1377)

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Met Leu Pro
1

ttt gcc tcc tgc ctc ccc ggg tct ttg ctg ctc tgg gcg ttt ctg ctg Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu	5 10 15	105
ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu Pro Asp Ser	20 25 30 35	153
tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His	40 45 50	201
tgc cgg gat gtc aac gag tgc ctg acc atc ccg gag gct tgc aag ggt Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly	55 60 65	249
gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc Glu Met Lys Cys Ile Asn His Tyr Gly Tyr Leu Cys Leu Pro Arg	70 75 80	297
tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro	85 90 95	345
gcg gcc cat gct caa caa cca aac cct tgc ccg cag ggc tac gag cct Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly Tyr Glu Pro	100 105 110 115	393
gat gaa cag gag agc tgt gtg gat gtg gac gag tgt acc cag gct ttg Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr Gln Ala Leu	120 125 130	441
cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro Gly Ser Tyr	135 140 145	489
cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val	150 155 160	537
gac ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn	165 170 175	585
ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly	180 185 190 195	633
cct aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala	200 205 210	681
cca tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg	215 220 225	729
tgt aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp	230 235 240	777
atc gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val	245 250 255	825

aac gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu 260 265 270 275	873
ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala 280 285 290	921
cac caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr 295 300 305	969
cgc tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser 310 315 320	1017
gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln 325 330 335	1065
cct tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser 340 345 350 355	1113
gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly 360 365 370	1161
gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe 375 380 385	1209
tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg 390 395 400	1257
cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr 405 410 415	1305
atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr 420 425 430 435	1353
gtc ttt gtg gga gcc tat acc ttc tgaagaccct cagggaaaggg ccatgtgggg Val Phe Val Gly Ala Tyr Thr Phe 440	1407
cccccttccc cctcccatag cttaaaggcagc cccggggggcc tagggatgac cgttctgctt	1467
aaaggaacta tgatgtgaag gacaataaag ggagaaaagaa ggaaaa	1513

<210> 16

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

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20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro
85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly
100 105 110

Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
210 215 220

Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
275 280 285

Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val
305 310 315 320

Gln Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
435 440

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide 3' hMBP1

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<210> 18		
<211> 21		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> oligonucleotide 5' hMBP1		
<400> 18		21
tgttagctact ccagctacct c		
<210> 19		
<211> 1122		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Human MBP1 cDNA (partial sequence)		
<400> 19		60
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cttgggatca gcttctcctc aggattctga agagcccgac agctacacgg aatgcacaga		180
tggctatgag tgggacccag acagccagca ctgcccggat gtcaacgagt gtctgaccat		240
ccctgaggcc tgcaaggggg aaatgaagt catcaaccac tacggggct acttgtgcct		300
gccccgctcc gctgccgtca tcaacgacct acacggcgag ggaccccccgc caccagtgcc		360
tcccgtctaa caccccaacc cctgcccacc aggctatgag cccgacgatc aggacagctg		420
tgtggatgtg gacgagtgtg cccagggcct gcacgactgt cgccccagcc aggactgcca		480
taacttgccct ggctcctatc agtgcacctg ccctgatggt taccgcaaga tcgggcccga		540
gtgtgtggac atagacgagt gccgctacccg ctactgccag caccgctgct tgaacctgcc		600
tggctccctc cgctgccagt gcgagccggg cttccagctg gggcctaaca accgctccctg		660
tgttgatgtg aacgagtgtg acatgggggc cccatgcgag cagcgtct tcaactccta		720
tgggaccttc ctgtgtcgct gccaccagg ctatgagctg catcgggatg gcttctcctg		780
cagtgatatt gatgagtgt a gctactccag ctacctctgt cagtaccgct gcgtcaacga		840
gccaggccgt ttctcctgcc actgcccaca gggttaccag ctgctggcca cacgcctctg		900

ccaagacatt	gatgagtgtg	agtctggtgc	gcaccagtgc	tccgaggccc	aaacctgtgt	960
caacttccat	ggggctacc	gctgcgtgga	caccaaccgc	tgcgtggagc	cctacatcca	1020
ggtctctgag	aaccgctgtc	tctgccccgc	ctccaaccct	ctatgtcgag	agcagccttc	1080
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<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

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tgtgagtctg	gtgcgcacca	gtgctccgag	gccccaaacct	gtgtcaactt	ccatggggcc	180
taccgctgctg	tggacaccaa	ccgctgcgtg	gagccctaca	tccaggtctc	tgagaaccgc	240
tgtctctgcc	cggcctccaa	ccctctatgt	cgagagcagc	tttcatccat	tgtgcaccgc	300
tacatgacca	tcaccccgaa	gcggagcgtg	cccgctgacg	tgttccagat	ccaggcgcacc	360
tccgtctacc	ccgggtgccta	caatgccttt	cagatccgtg	ctggaaaactc	gcagggggac	420
ttttacatta	ggcaaataaa	caacgtcagc	gccatgctgg	tcctcgcccg	gccgggtgacg	480
ggccccccggg	agtacgtgct	ggacctggag	atggtcacca	tgaattccct	catgagctac	540
cggggccagct	ctgtactgag	gctcaccgtc	ttttagggg	cctacacctt	ctgaggagca	600
ggagggagcc	accctccctg	cagctaccct	agctgaggag	cctgttgtga	ggggcagaat	660
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<210> 21

<211> 1480

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<220>

<221> CDS

<222> (59)..(1387)

<400> 21

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58

atg ctc ccc tgc gcc tcc tgc cta ccc ggg tct cta ctg ctc tgg gcg Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala	106
1 5 10 15	
ctg cta ctg ttg ctc ttg gga tca gct tct cct cag gat tct gaa gag Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu	154
20 25 30	
ccc gac agc tac acg gaa tgc aca gat ggc tat gag tgg gac cca gac Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp	202
35 40 45	
agc cag cac tgc cgg gat gtc aac gag tgt ctg acc atc cct gag gcc Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala	250
50 55 60	
tgc aag ggg gaa atg aag tgc atc aac cac tac ggg ggc tac ttg tgc Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys	298
65 70 75 80	
ctg ccc cgc tcc gct gcc gtc atc aac gac cta cac ggc gag gga ccc Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro	346
85 90 95	
ccg cca cca gtg cct ccc gct caa cac ccc aac ccc tgc cca cca ggc Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly	394
100 105 110	
tat gag ccc gac gat cag gac agc tgt gtg gat gtg gac gag tgt gcc Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala	442
115 120 125	
cag gcc ctg cac gac tgt cgc ccc agc cag gac tgc cat aac ttg cct Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro	490
130 135 140	
ggc tcc tat cag tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro	538
145 150 155 160	
gag tgt gtg gac ata gac gag tgc cgc tac cgc tac tgc cag cac cgc Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg	586
165 170 175	
tgc gtg aac ctg cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe	634
180 185 190	
cag ctg ggg cct aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp	682
195 200 205	
atg ggg gcc cca tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe	730
210 215 220	
ctg tgt cgc tgc cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser	778
225 230 235 240	
tgc agt gat att gat gag tgt agc tac tcc agc tac ctc tgt cag tac Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr	826
245 250 255	

cgc tgc gtc aac gag cca ggc cgt ttc tcc tgc cac tgc cca cag ggt Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly 260 265 270	874
tac cag ctg ctg gcc aca cgc ctc tgc caa gac att gat gag tgt gag Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu 275 280 285	922
tct ggt gcg cac cag tgc tcc gag gcc caa acc tgt gtc aac ttc cat Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His 290 295 300	970
ggg ggc tac cgc tgc gtg gac acc aac cgc tgc gtg gag ccc tac atc Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile 305 310 315 320	1018
cag gtc tct gag aac cgc tgt ctc tgc ccg gcc tcc aac cct cta tgt Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys 325 330 335	1066
cga gag cag cct tca tcc att gtg cac cgc tac atg acc atc acc tcg Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser 340 345 350	1114
gag cgg agc gtg ccc gct gac gtg ttc cag atc cag gcg acc tcc gtc Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val 355 360 365	1162
tac ccc ggt gcc tac aat gcc ttt cag atc cgt gct gga aac tcg cag Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln 370 375 380	1210
ggg gac ttt tac att aggcaa atc aac aac gtc agc gcc atg ctg gtc Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val 385 390 395 400	1258
ctc gcc cgg ccg gtg acg ggc ccc cgg gag tac gtg ctg gac ctg gag Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu 405 410 415	1306
atg gtc acc atg aat tcc ctc atg agc tac cgg gcc agc tct gta ctg Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu 420 425 430	1354
agg ctc acc gtc ttt gta ggg gcc tac acc ttc tgaggagc gagggagcca Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe 435 440	1407
ccctccctgc agctacccta gctgaggagc ctgttgtgag gggcagaatg agaaaggcaa	1467
taaaggaga aag	1480

<210> 22
<211> 443
<212> PRT
<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<400> 22

Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala
1 5 10 15

Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro
85 90 95

Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly
100 105 110

Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
210 215 220

Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
275 280 285

Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile
305 310 315 320

Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Phe Ala Met Leu Val
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
435 440

<210> 23

<211> 817

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 cDNA (partial sequence)

<400> 23
gctgtggcag aaacccctga cttctgccca ccacctccca gcctcaggat gctcccttt 60
gcctcctgcc tccccgggtc tttgctgctc tggcggttc tgctgttgct cttggggagca 120
gcgtccccac aggatcccga ggagccggac agtacacgg aatgcacaga tggctatgag 180
tgggatgcag acagccagca ctgcccggat gtcaacgagt gcctgaccat cccggaggct 240
tgcaagggtg agatgaaatg catcaaccac tacgggggtt atttgtgtct gcctcgctct 300
gctgccgtca tcagtgtatct ccatggtaa ggacctccac cgccagcggc ccatgctcaa 360
caaccaaacc cttgcccga gggctacgag cctgtatgaac aggagagctg tgtggatgtg 420
gacgagtgtta cccaggctt gcatgactgt cgccttagtc aggactgcca taaccttcct 480
ggctcctacc agtgcacctg ccctgatggt taccgaaaaa ttggaccgcga atgtgtggac 540
atagatgagt gtcgttaccg ctattgccag catcgatgtg tgaacctgcc gggctcttt 600
cgatgccagt gtgagccagg cttccagttg ggacctaaca accgccttg tgtggatgtg 660
aatgagtgtg acatgggagc cccatgtgag cagcgctgct tcaactccta tgggaccttc 720
ctgtgtcgtc gtaaccaggc ctatgagctg caccggatg gcttctcctg cagcgatatc 780
gatgagtgcg gctactccag ttacctctgc cagtacc 817

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-GAPDH oligonucleotide

<400> 24

cggagtcaac ggatttggtc gtat

24

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-GAPDH oligonucleotide

<400> 25

agccttctcc atgggtgtga agac

24

<210> 26
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> antisense-beta-actin oligonucleotide

<400> 26
cggttggcct tggggttcag ggggg 25

<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> sense-MBP1 oligonucleotide

<400> 27
gccctgatgg ttacccgcaag a 21

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> antisense MBP1 oligonucleotide

<400> 28
agcccccatg gaaggttgaca c 21

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> sense-beta-actin oligonucleotide

<400> 29

gtggggcgcc ccagggacca

20

<210> 30

<211> 1358

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<220>

<221> CDS

<222> (1)..(885)

<400> 30

tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc gag tgc gac
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

48

ata gac gag tgc cgc tac cgc tac tgc cag cac cgc tgc gtc aac ctg
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

96

cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc cag ctg ggg cct
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

144

aac aac cgc tcc tgt gtt gat gtg aac gag tgc gac atg ggg gcc cca
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

192

tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgc
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

240

cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc tgc agt gat att
His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
85 90 95

288

gat gag tgt agc tac tcc agc tac ctc tgt cag tac cgc tgc gtc aac
Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
100 105 110

336

gag cca ggc cgt ttc tcc tgc cac tgc cca cag ggt tac cag ctg ctg
Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
115 120 125

384

gcc aca cgc ctc tgc caa gac att gat gag tgt gag tct ggt gcg cac
Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His
130 135 140

432

cag tgc tcc gag gcc caa acc tgt gtc aac ttc cat ggg ggc tac cgc
Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145 150 155 160

480

tgc gtg gac acc aac cgc tgc gtg gag ccc tac atc cag gtc tct gag
Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu
165 170 175

528

aac cgc tgt ctc tgc ccg gcc tcc aac cct cta tgt cga gag cag cct
Page 20

576

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro					
180	185	190			
tca tcc att gtg cac cgc tac atg acc atc acc tcg gag cg _g agc gtg Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val	195	200	205	624	
ccc gct gac gtg ttc cag atc cag gc _g acc tcc gtc tac ccc ggt gcc Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala	210	215	220	672	
tac aat gcc ttt cag atc cgt gct gga aac tcg cag ggg gac ttt tac Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr	225	230	235	240	720
att agg caa atc aac aac gtc agc gcc atg ctg gtc ctc gcc cg _g ccg Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro	245	250	255	768	
gtg acg ggc ccc cg _g gag tac gtg ctg gac ctg gag atg gtc acc atg Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met	260	265	270	816	
aat tcc ctc atg agc tac cg _g gcc agc tct gta ctg agg ctc acc gtc Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val	275	280	285	864	
ttt gta ggg gcc tac acc ttc tgaggagcag gagggagcca ccctccctgc Phe Val Gly Ala Tyr Thr Phe	290	295		915	
agctacccta gctgaggagc ctgttgtgag gggcagaatg agaaaggcaa taaaaggaga aagaaaagtcc tgggtggctga ggtggggcggg tcacactgca ggaaggctca ggctggggca				975	
gggtggcact tgggggggca ggccaagttc acctaaatgg gggtctctat atgttcaggc ccaggggccc ccattgacag gagctggag ctctgcacca cgagcttcag tcaccccgag				1035	
aggagaggag gtaacgagga gggcggactc caggccccgg cccagagatt tggacttggc tggcttgcaag gggctctaag aaactccact ctggacagcg ccaggaggcc ctgggttcca				1095	
ttcctaactc tgcctcaaac tgtacattt gataagccct agtagttccc tggcctgtt tttctataaa acgaggcaac tgg				1155	
				1215	
				1275	
				1335	
				1358	

<210> 31

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<400> 31

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
85 90 95

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145 150 155 160

cys val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
180 185 190

Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
245 250 255

val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
275 280 285

Phe Val Gly Ala Tyr Thr Phe
290 295

<210> 32

<211> 1663

<212> DNA

<213> Artificial Sequence

<220>
<223> murine fibulin 2 c-term fragment

<220>

<221> CDS

<222> (1)..(999)

<400> 32

gag ggc tct gaa tgt gtg gat gtg aat gag tgg gag aca ggt gtg cat
Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His
1 5 10 15

48

cgc tgt ggc gag ggc caa ctg tgc tat aac ctc cct gga tcc tac cgc
Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg
20 25 30

96

tgt gac tgc aag ccc ggc ttc cag agg gat gca ttc ggc agg act tgc
Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys
35 40 45

144

att gat gtg aac gaa tgc tgg gtc tcg ccg ggc cgc ctg tgc cag cac
Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His
50 55 60

192

aca tgt gag aac aca ccg ggc tcc tac cgc tgc tcc tgc gct gct ggc
Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly
65 70 75 80

240

ttc ctt ttg gcc gca gat ggc aaa cat tgt gaa gat gtg aac gag tgc
Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys
85 90 95

288

gag act cgg cgc tgc agc cag gaa tgt gcc aac atc tat ggc tcc tat
Glu Thr Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr
100 105 110

336

cag tgc tac tgc cgt cag ggc tac cag ctg gca gag gat ggg cat acc
Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr
115 120 125

384

tgc aca gac atc gat gag tgt gca cag ggc gcg ggc att ctc tgt acc
Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr
130 135 140

432

ttc cgc tgt gtc aac gtg cct ggg agc tac cag tgt gca tgc cca gag Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu 145 150 155 160	480
caa ggg tat aca atg atg gcc aac ggg agg tcc tgc aag gac ctg gat Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp 165 170 175	528
gag tgt gca ctg ggc acc cac aac tgc tct gag gct gag acc tgc cac Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His 180 185 190	576
aat atc cag ggg agt ttc cgc tgc ctg cgc ttt gat tgt cca ccc aac Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn 195 200 205	624
tat gtc cgt gtc tca caa acg aag tgc gag cgc acc aca tgc cag gat Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp 210 215 220	672
atc acg gaa tgt caa acc tca cca gct cgc atc acg cac tac cag ctc Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu 225 230 235 240	720
aat ttc cag aca ggc cta ctg gta cct gca cat atc ttc cgc atc ggc Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly 245 250 255	768
cct gct ccc gcc ttt gct ggg gac acc atc tcc ctg acc atc acg aag Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys 260 265 270	816
ggc aat gag gag ggc tac ttc gtc aca cgc aga ctc aat gcc tac act Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr 275 280 285	864
ggg gta tcc ctg cag cgg tct gtt ctg gag cgg cgg gac ttt gcc Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala 290 295 300	912
cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe 305 310 315 320	960
ctg gcc aag atg tac atc ttc ttc acc act ttt gcc cca tgaggtgaca Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro 325 330	1009
tgtcaggcaa tccctccagg tgatgcctgg gcggggca gctgcgccac tcctaagtgg cttttgctg tgactctgta acttaactta atcatgctga gctgggttgt cttgagtctc	1069
tacccttagag ggagggagat gcaccccagc aggcactgag tacaggccag ggtcacccga	1129
ggcttagatgg tgacctgcaa actggaaaca gccatagggg gcttctgaac tccactcctc	1189
aactatggct acagctgaca ttccattcct tcattccactg tgttcctcaa taaaaaaaaa	1249
aaatcagctg tgcatggtag cacagacctt taatcctagc actggggagg cagaggtagg	1309
tagatctctg agttccaggc cagcctggc tacactggga gttctaacca gccagagcta	1369
catagagaga ccctatctca acaaggaaaa aacgaaagaa atctctgtga gttccaggcc	1429
	1489

agcctggtct acgctggag ttcttaaccag ccagagctac atagagagat cctatctcaa 1549
caaggaaaaa tgaaagaaat cattttaaa ggtttttt tttgctgttg ttgtttaatg 1609
ataagatcg cacatataca ttattaaaaa tgatcaaata gcacagaaag gtta 1663

<210> 33

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine fibulin 2 c-term fragment

<400> 33

Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His
1 5 10 15

Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg
20 25 30

Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys
35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His
50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly
65 70 75 80

Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys
85 90 95

Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr
100 105 110

Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr
115 120 125

cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr
130 135 140

Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu
145 150 155 160

Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp
165 170 175

Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His
180 185 190

Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn
195 200 205

Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp.
210 215 220

Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu
225 230 235 240

Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly
245 250 255

Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys
260 265 270

Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr
275 280 285

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala
290 295 300

Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe
305 310 315 320

Leu Ala Lys Met Tyr Ile Phe Phe Thr Phe Ala Pro
325 330

App. No. 09/829,936

Filing Date: April 11, 2001

Inv: Emmanuel CONSEILLER, et al.

Title: Polypeptide (MBP1) Capable of
Interacting With Oncogenic Mutants
of the p53 Protein

Attny. Ref. No. ST98033

CORRECTED SEQUENCE LISTING

Recorded: May 21, 2003